SEQUENCE LISTING

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<110>  Dynan, William
       Takeda, Yoshihiko
       Li, Shuyi

<120>  Compositions and Methods for Modulating DNA Repair

<130>  791301-1010

<160>  36

<170>  PatentIn version 3.2

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<220>
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Pro Lys Lys Lys Arg Lys Val Cys
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<400>  2

Gly Lys Lys Lys Tyr Lys Leu Lys His
1               5


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Lys Ser Lys Lys Lys Ala Gln
1               5


<210>  4
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Lys Glu Leu Lys Gln Lys Gln Ile Thr Lys
1               5               10


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Asn Glu Trp Thr Leu Glu Leu Leu Glu Glu Leu Lys Asn Glu Ala Val
1               5               10              15


Arg His Phe


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<400>  6

Arg His Ser Arg Ile Gly Val Thr Arg Gly Arg Arg Ala Arg Asn Gly
1               5               10              15


Ala Ser Arg Ser
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Arg Lys Lys Arg Arg Gln Arg Arg Arg
1   5

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<400> 8

Arg Gln Ala Arg Arg Asn Arg Arg Arg Trp Arg
1   5   10

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<400> 9

Gly Lys Lys Arg Ser Lys Val
1   5

<210> 10
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Lys Ser Arg Lys Arg Lys Leu
1   5

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Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys Leu
1               5               10              15
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Asp Lys


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1               5               10              15
```

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Lys Lys Ser Lys
            20
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<400>  13
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Lys Lys Tyr Glu Asn Val Val Ile Lys Arg Ser Pro Arg Lys Arg Gly
1               5               10              15
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```
Arg Pro Arg Lys
            20
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His Ile Val Thr Ala Thr Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg
1               5               10              15
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Arg

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Arg Lys Lys Arg Arg Gln Arg Arg Arg
1   5

<210> 16
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Lys Lys Tyr Ile Glu Ile Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly
1   5   10   15

Asp Ser Asp Gly Pro Ser Tyr Met
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<220>
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<400> 17

Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Leu Ser Cys Lys Ala Phe Asp Tyr Thr Phe Thr Thr Tyr
            20   25   30

Asp Ile Asn Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Trp Ile Gly

```
                   35                      40                      45

 5     Trp Ile Tyr Pro Gly Ser Gly Asn Asn Lys Tyr Asn Glu Lys Phe Lys
           50              55                  60


       Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Arg Ala Ala Tyr Met
       65              70                  75                      80
10

       His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
                       85                  90                  95

15
       Gly Gly Pro Leu Asn Met Thr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
                   100             105                 110·

20     Thr Val Thr Val Ser Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ser
               115                 120                 125


       Met Tyr Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser
25         130             135                 140


       Gln Asp Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys
       145             150                 155                 160
30

       Ser Pro Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val
                   165                 170                 175

35
       Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr
                   180             185                 190


40     Ile Ser Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln
           195             200                 205


       Tyr Asp Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
45         210             215                 220


       Lys Arg
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Phe Thr Thr Tyr Asp Ile Asn
1   5

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<220>
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<400> 19

Trp Ile Tyr Pro Gly Ser Gly Asn Asn Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 20
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<220>
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<400> 20

Gly Pro Leu Asn Met Thr Gly Phe Asp Tyr
1   5   10

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<400> 21

Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser
1   5   10

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<220>
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<400> 22

Arg Ala Asn Arg Leu Val Asp
1   5

<210> 23
<211> 9
<212> PRT
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<220>
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<400> 23

Leu Gln Tyr Asp Glu Leu Pro Leu Thr
1   5

<210> 24
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dccgggatcc ccaagcttcc tccagtctgt tgcaag
36

<210> 25
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<400> 25
dcaagcggcc gccaatataa attgaccatt cttctag
37

<210> 26
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<220>

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<223>  Primer

<400>  26
dcggggatcc ttggcagaag taggcctgaa tgctc
35
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dgaagcggcc gcctacattc tctcgccaat gaacg
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cggggatccc cattcagcct gcaggccacg cta
33
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dggggcggcc gctcaattcc aacaacatag ggctt
35
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dgggggatcc ccgcggttca ataattatgt ggactgc
37
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dcaagcggcc gcctcttttt ggatgaaaga catgtttc
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dgggggatcc ggggtcccta aagatgaagt gttagc
36


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dgaagcggcc gcagttatcc acctcgtccc ctggaag
37


<210>   34
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Leu Ala Asp Ser Thr Leu Ser Glu Glu Met Ser Gln Phe Asp Phe Ser
1               5                   10                  15

Thr Gly Val Gln Ser Tyr Ser Tyr Ser
            20                  25
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<210> 35
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dcttcgaatt ctgcaggtga agctgcagga
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15

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25   dgtggatccc gcggttccag cggatccg
28